

Fig. 1

a0022 (LIP9)

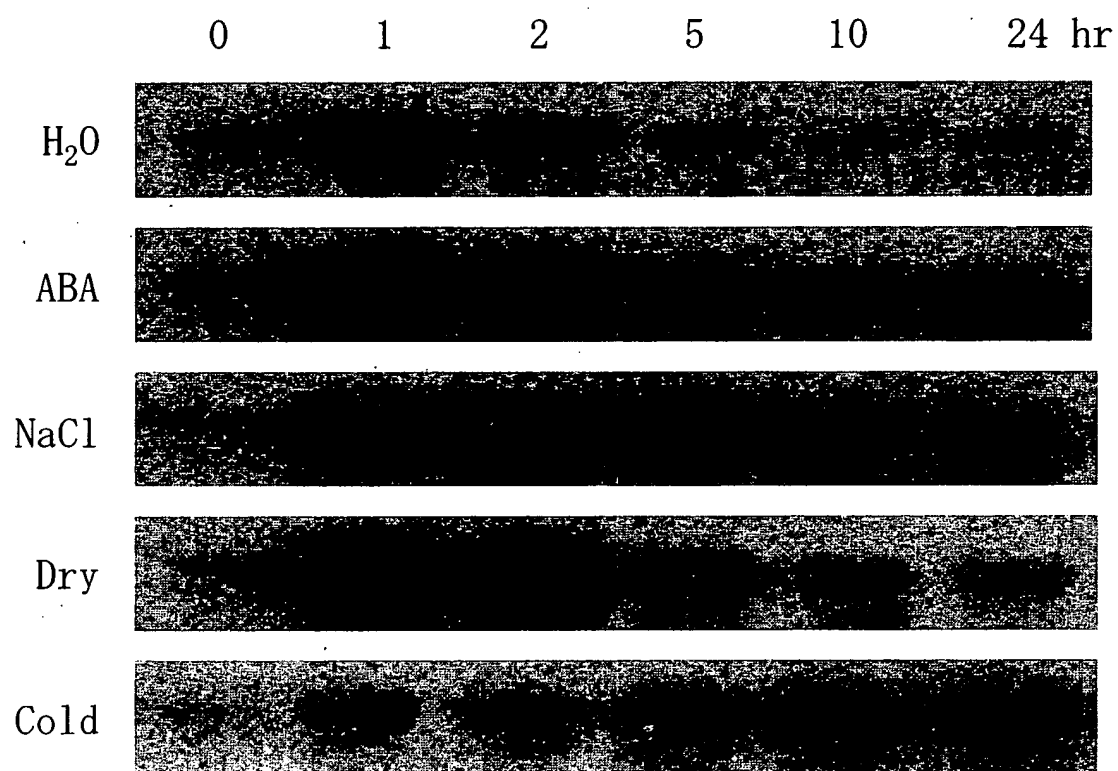


Fig. 1

a0022 (LIP9)

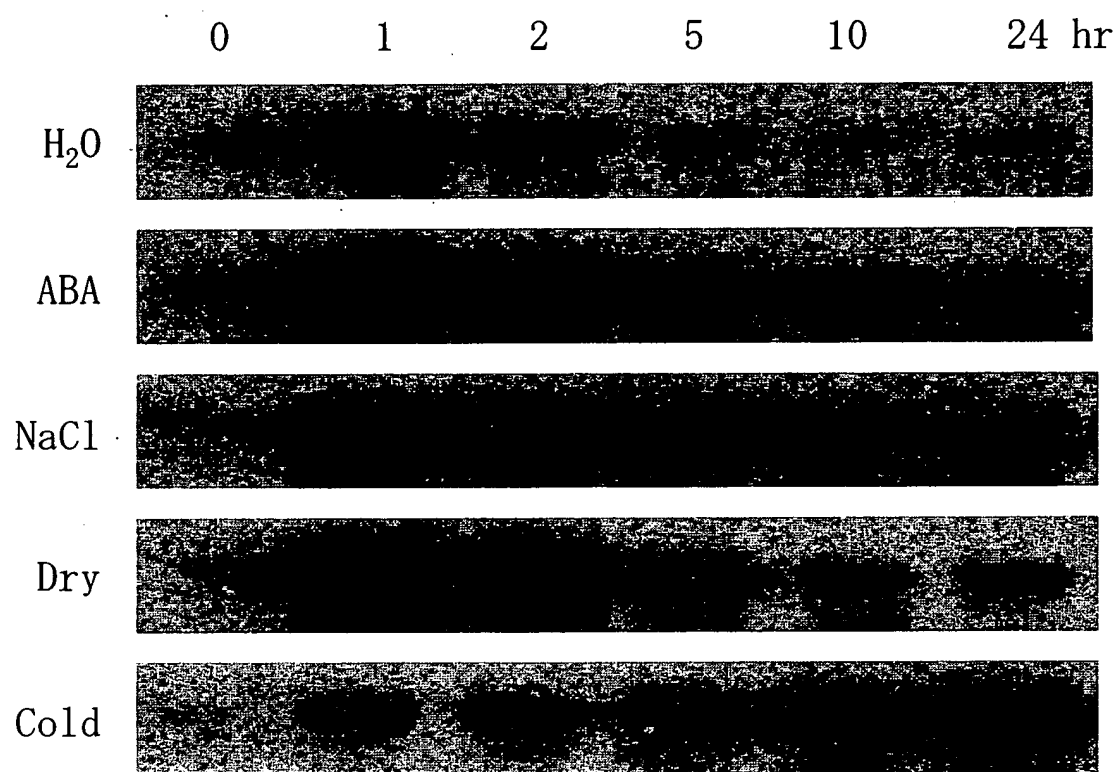


Fig. 1

a0022 (LIP9)

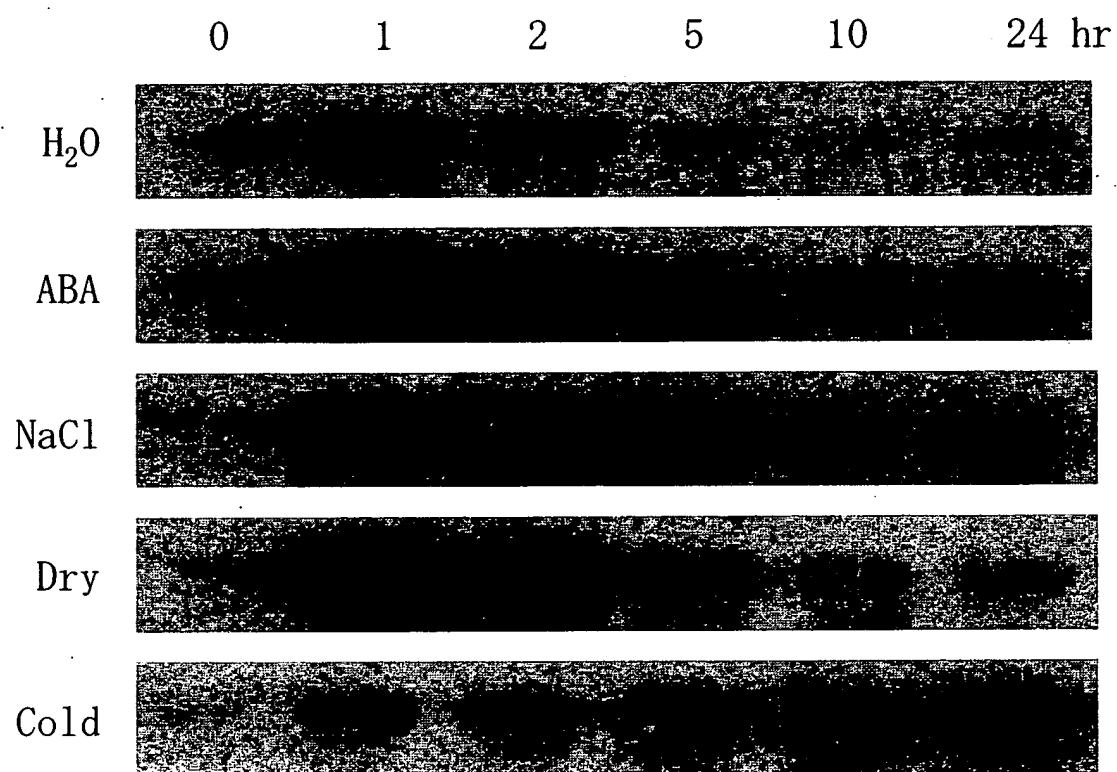


Fig. 2

LIP 9

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      10      20      30      40      50      60
TCATCAGCTA TCATCAAAGC GAAGGAAAGA AAGAAAAATA AAAGGAAAAG AACTGGCTGG

      70      80      90     100     110     120
AAATTAGAGA AGCCCCGGAC GACTCGATCT GGGGGTGGCA AATTAATCAG TGTGATCAAC Myb

      130     140     150     160     170     180
AGGGATAACT TATCCCGTCC GACCAAATCC ACCAACCAAA CCAAGACCCG ATTTGTTAGG

      190     200     210     220     230     240
CTGTGAAAGA CGGATCAGTG GGACCCTGAT CTACGGACCC CATATGTCAC CGTCCAGGTC

      250     260     270     280     290     300
TCTGGATCTC TCCCGTCGTC CTAATCAGAC ACCGCGCGCG CGGTGCCGTC GCTCTCGAGC

      310     320     330     340     350     360
CGTGTCCCGC TCCCAACTCG TCACAAAAGC GATCACAGAC TCTTCCTTCC TCTGCTGGGA

      370     380     390     400     410     420
GAGAAGAAAA ATTGGCCGCG ATGATGCCGA TAAAGAGGAA AAAGGGATGA GAATCCGATG

      430     440     450     460     470     480
GAAAAAAACT GATGTTAATC TATCGTACT GCTGCGCACT AAGACGAATC GTATCCGAAC

      490     500     510     520     530     540
AAGAAACGCT TACGTTACTG TTCCTAAATG GATCGCTCCG CTCATCACTT AACCAAAAAT

      550     560     570     580     590     600
CGATTAGGAA ATTGACGGAC AGCGACGCC GAAGCCAAGT GTCTCGTCGC GTAGGCGTCG

      610     620     630     640     650     660
AGGCCTCGAA GCAGAGGGAG CGGAGAGGCG GACGCGCCGC CCACGCCTCC TCTCCCTCGG

      670     680     690     700     710     720
TGACACGGCC GTCTGGCTCC ACATGGCGCC GACCTCTCCC GATGCGTCCA CCCGTCCCGA

      730     740     750     760     770     780
GGCACCGCCA CGTCGGAACC AGCCGGCCGC CCCACGCGAT TGCCGACACG CGTCGCGGCG

      790     800     810     820     830     840
CCACTGGCTC ACCCGCTGCC TGCCTCTGCC TGCCCCCAT CTCGTCGCCA TTTCCCGCCC

      850     860     870     880     890     900
ACGCTTCTTG TCCTCGCGTC GCCTACGCGT ACGTACGATA CAAACGCCGC ACCTTTCGAT

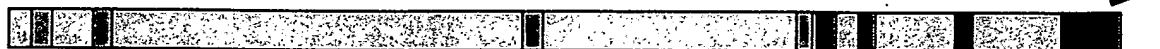
      910     920     930     940     950     960
CCCCTCCGCT ATATAAGGAG GGCATCTGCC TCGCCACCTT CTTATCCGA AAGCAAAAGC

      970     980     990     1000    1010    1020
GACTCGTCAC AGCTCAAACA AGTCAAGAGC GAATAGTTCT TGCTGATCTG TTGTTTGATT

      1030    1040    1050    1060    1070    1080
ACTTTAGTTC TCGAGAGGCT TTAGCTGAAT CCATCGATCA TGGAGGATGA GAGGAACA.

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LIP 9



DRE  
 (A/ GCCGAC)
  Myb
  Myc
  TATA

Fig. 3

LIP9: Gus construct

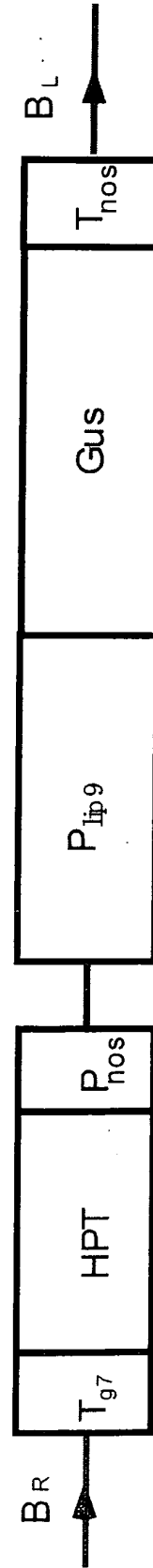


Fig. 4

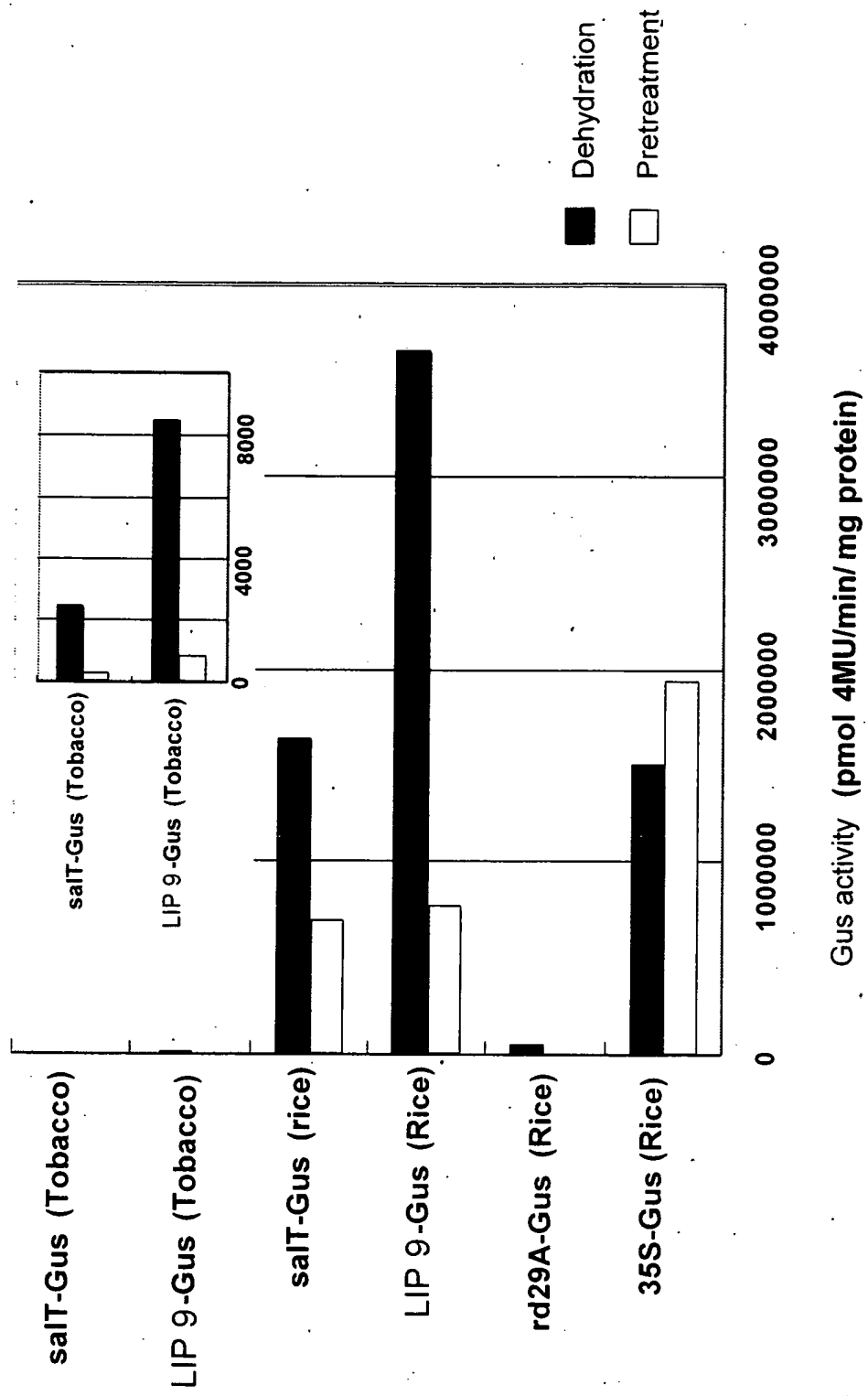
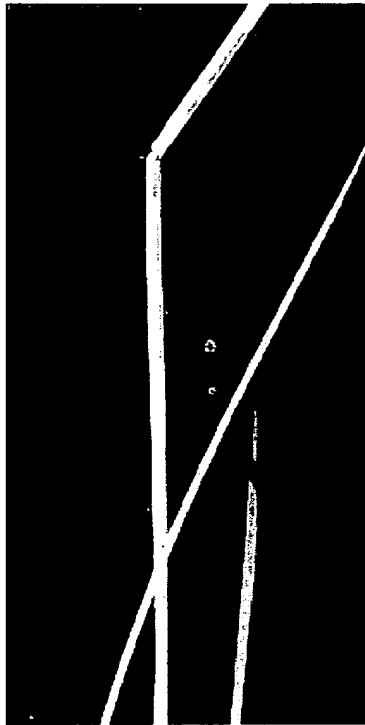


Fig. 5

Leaves



Roots

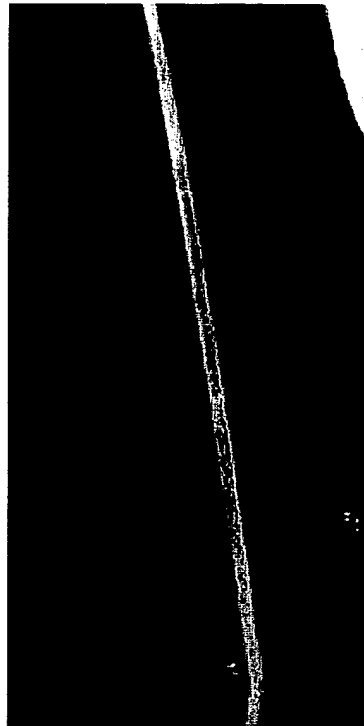
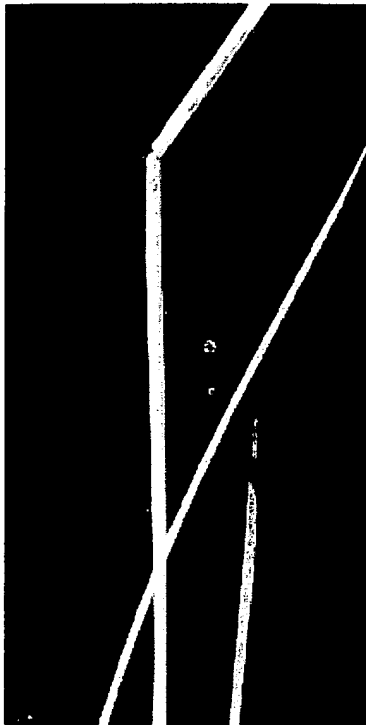


control

Salt stress

Fig. 5

Leaves



Roots



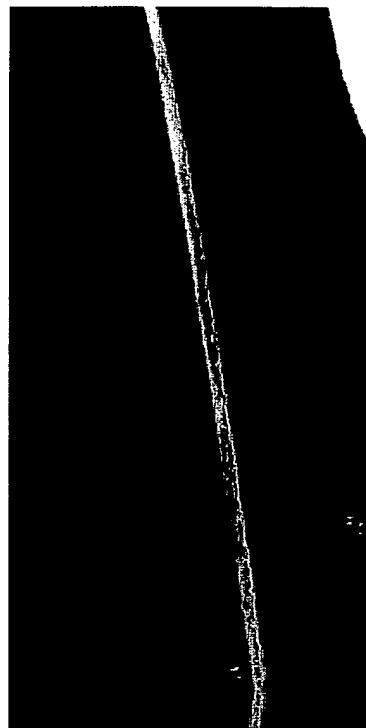
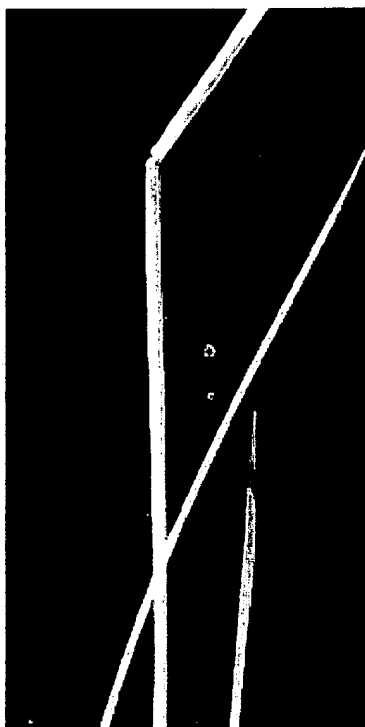
control

Salt stress



Fig. 5

Leaves



Roots

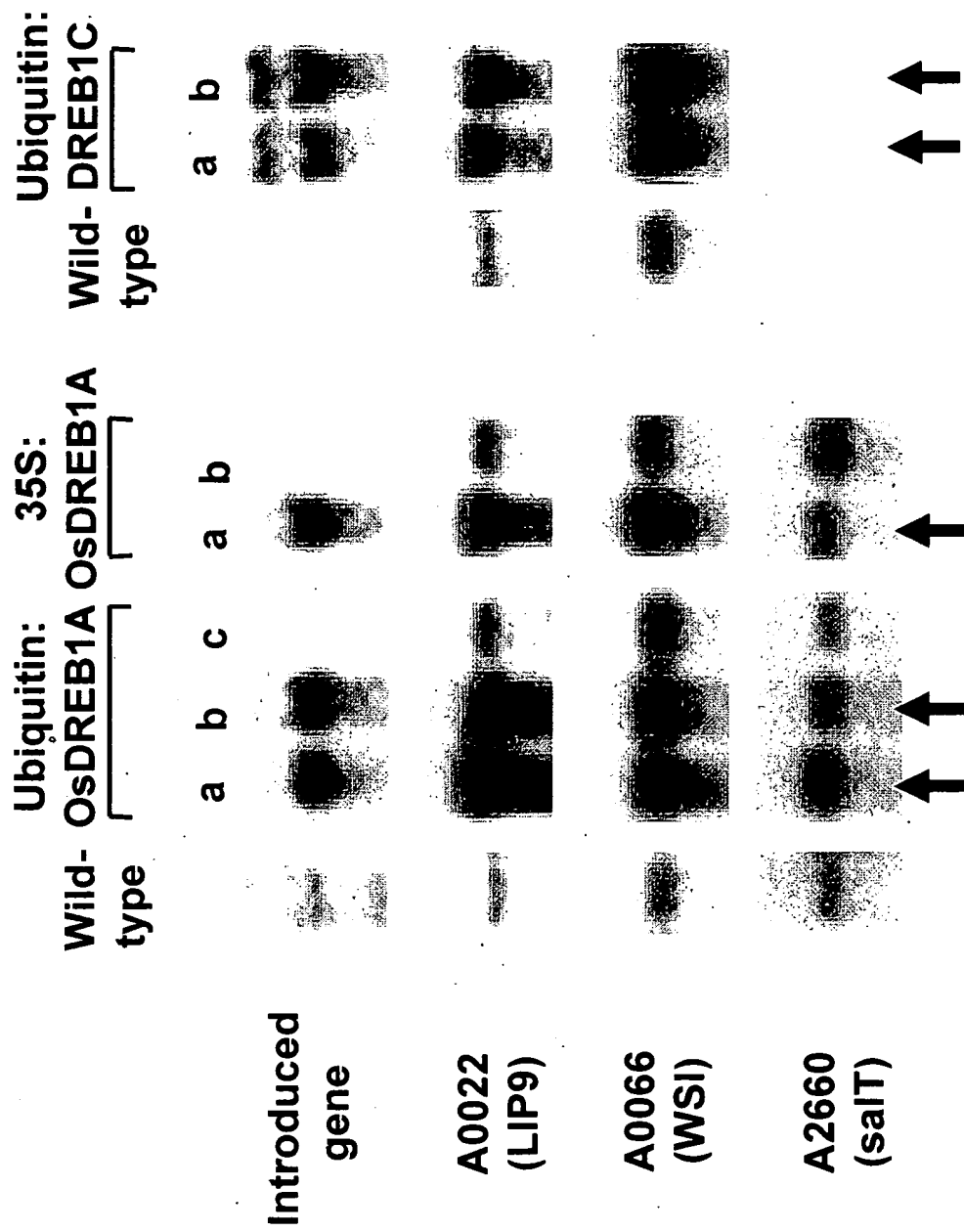


control

Salt stress



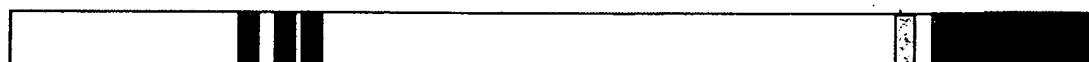
Fig. 6





WSI724

WSI724



**ORF**

Fig. 8

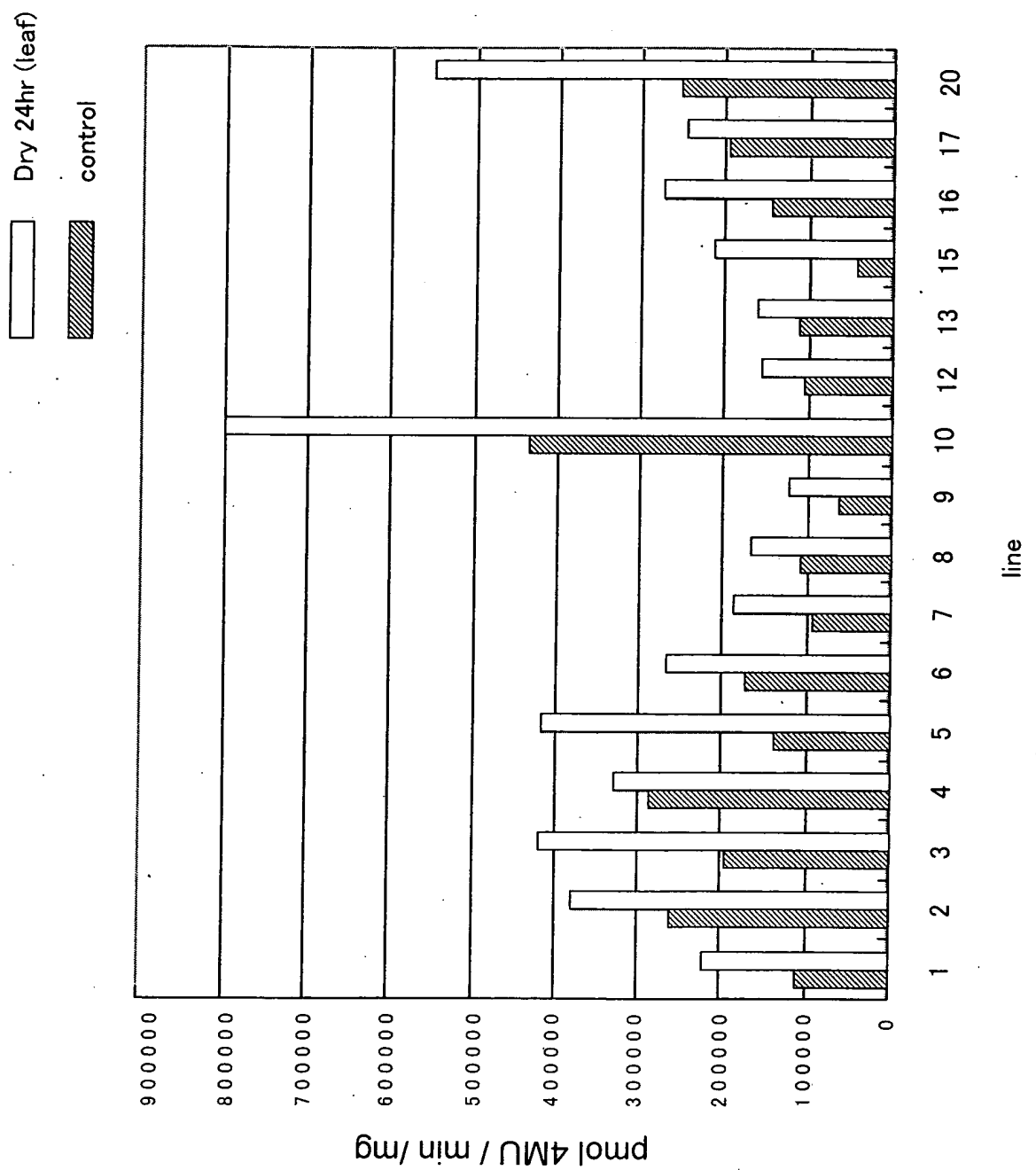


Fig. 9

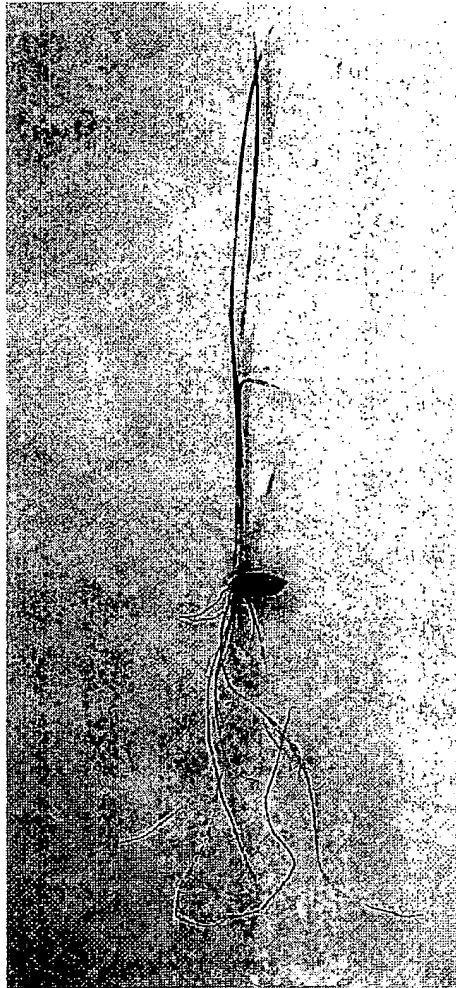


Fig. 9

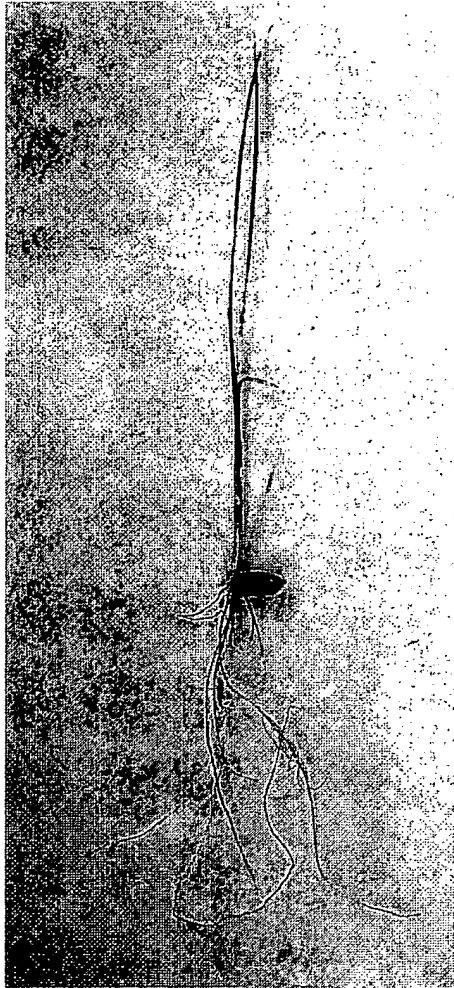




Fig. 9

